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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
- (ii) TITLE OF INVENTION: Bacterial Superantigen
Vaccines
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Charles H. Harris
 - (B) STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
 - (C) CITY: FORT DETRICK
 - (D) STATE: MARYLAND
 - (E) COUNTRY: USA
 - (F) ZIP: 21702-5012
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.5
 - (D) SOFTWARE: Microsoft Word 6.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/882,431
 - (B) FILING DATE: June 25, 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Charles H. Harris
 - (B) REGISTRATION NUMBER: 34,616
 - (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: (301) 619-2065
 - (B) TELEFAX: (301) 619-7714

(2) INFORMATION FOR SEQUENCE ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 830
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAAAAAA CAGCATTTAC ATTACTTTTA TTCATTGCCC	40
TAACGTTGAC AACAAAGTCCA CTTGTAAATG GTAGCGAGAA	80
AAGCGAAGAA ATAAATGAAA AAGATTTGCG AAAAAAGTCT	120
GAATTGCAGG GAACAGCTTT AGGCAATCTT AAACAAATCT	160
ATTATTACAA TGAAAAAGCT AAAACTGAAA ATAAAGAGAG	200
TCACGATCAA TTTCGACAGC ATACTATATT GTTTAAAGGC	240
TTTTTTTACAG ATCATTCGTG GTATAACGAT TTATTAGTAC	280
GTTTTTGATTC AAAGGATATT GTTGATAAAT ATAAAGGGAA	320
AAAAGTAGAC TTGTATGGTG CTTATGCTGG TTATCAATGT	360
GCGGGTGGTA CACCAAACAA AACAGCTTGT ATGTATGGTG	400
GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA	440
AAAAGTGCCG ATCAATTTAT GGCTAGACGG TAAACAAAAT	480
ACAGTACCTT TGGAAACGGT TAAAACGAAT AAGAAAAATG	520
TAAGTGTTC GGAGTTGGAT CTTCAAGCAA GACGTTATTT	560
ACAGGAAAAA TATAATTTAT ATAACTCTGA TGTTTTTGAT	600
GGGAAGGTT AGAGGGGATT AATCGTGTTT CATACTTCTA	640
CAGAACCTTC GGTTAATTAC GATTTATTTG GTGCTCAAGG	680
ACAGTATTCA AATACACTAT TAAGAATATA TAGAGATAAT	720
AAAACGATTA ACTCTGAAAA CATGCATATT GATATATATT	760
TATATACAAG TTAAACATGG TAGTTTGGAC CAACGTAATG	800
TTCAGATTAT TATGAACCGA GAATAATCTA	830

(3) INFORMATION FOR SEQUENCE ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257

(B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Lys	Thr	Ala	Phe	Thr	Leu	Leu	Leu	1	5	10
Phe	Ile	Ala	Leu	Thr	Leu	Thr	Thr	Ser	Pro	15	20	
Leu	Val	Asn	Gly	Ser	Glu	Lys	Ser	Glu	Glu	25	30	
Ile	Asn	Glu	Lys	Asp	Leu	Arg	Lys	Lys	Ser	35	40	
Glu	Leu	Gln	Gly	Thr	Ala	Leu	Gly	Asn	Leu	45	50	
Lys	Gln	Ile	Tyr	Tyr	Tyr	Asn	Glu	Lys	Ala	55	60	
Lys	Thr	Glu	Asn	Lys	Glu	Ser	His	Asp	Gln	65	70	
Phe	Arg	Gln	His	Thr	Ile	Leu	Phe	Lys	Gly	75	80	
Phe	Phe	Thr	Asp	His	Ser	Trp	Tyr	Asn	Asp	85	90	
Leu	Leu	Val	Arg	Phe	Asp	Ser	Lys	Asp	Ile	95	100	
Val	Asp	Lys	Tyr	Lys	Gly	Lys	Lys	Val	Asp	105	110	
Leu	Tyr	Gly	Ala	Tyr	Ala	Gly	Tyr	Gln	Cys	115	120	
Ala	Gly	Gly	Thr	Pro	Asn	Lys	Thr	Ala	Cys	125	130	
Met	Tyr	Gly	Gly	Val	Thr	Leu	His	Asp	Asn	135	140	
Asn	Arg	Leu	Thr	Glu	Glu	Lys	Lys	Val	Pro	145	150	
Ile	Asn	Leu	Trp	Leu	Asp	Gly	Lys	Gln	Asn	155	160	

Thr Val Pro Leu Glu Thr Val Lys Thr Asn	
	165 170
Lys Lys Asn Val Thr Val Gln Glu Leu Asp	
	175 180
Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys	
	185 190
Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp	
	195 200
Gly Lys Val Gln Arg Gly Leu Ile Val Phe	
	205 210
His Thr Ser Thr Glu Pro Ser Val Asn Tyr	
	215 220
Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser	
	225 230
Asn Thr Leu leu Arg Ile Tyr Arg Asp Asn	
	235 240
Lys Thr Ile Asn Ser Glu Asn Met His Ile	
	245 250
Asp Ile Tyr Leu Tyr Thr Ser	
	255

(4) INFORMATION FOR SEQUENCE ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAGAAAAG CGAAGAAATA AATGAAAAAG ATTTGCGAAA	40
AAAGTCTGAA TTGCAGGGAA CAGCTTTAGG CAATCTTAAA	80
CAAATCTATT ATTACAATGA AAAAGCTAAA ACTGAAAATA	120
AAGAGAGTCA CGATCAATTT CGACAGCATA CTATATTGTT	160
TAAAGGCTTT TTTACAGATC ATTCGTGGTA TAACGATTTA	200

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TTAGTACGTT TTGATTCAAA GGATATTGTT GATAAATATA 240
AAGGGAAAAA AGTAGACTTG TATGGTGCTT ATGCTGGTTA 280
TCAATGTGCG GGTGGTACAC CAAACAAAAC AGCTTGTATG 320
TATGGTGGTG TAACGTTACA TGATAATAAT CGATTGACCG 360
AAGAGAAAAA AGTGCCGATC AATTTATGGC TAGACGGTAA 400
ACAAAATACA GTACCTTTGG AAACGGTTAA AACGAATAAG 440
AAAAATGTAA CTGTTACAGGA GTTGGATCTT CAAGCAAGAC 480
GTTATTTACA GGAAAAATAT AATTTATATA ACTCTGATGT 520
TTTTGATGGG AAGGTTCAGA GGGGATTAAT CGTGTTTCAT 560
ACTTCTACAG AACCTTCGGT TAATTACGAT TTATTTGGTG 600
CTCAAGGACA GTATTCAAAT ACACTATTAA GAATATATAG 640
AGATAATAAA ACGATTAACT CTGAAAACAT GCATATTGAT 680
ATATATTTAT ATACAAGTTA AACATGGTAG TTTTGACCAA 720
CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA 757

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(5) INFORMATION FOR SEQUENCE ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:233
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
      5                               10
Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly
      15                             20
Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
      25                             30
Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
      35                             40
Lys Glu Ser His Asp Gln Phe Arg Gln His
      45                             50

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Thr	Ile	Leu	Phe	Lys	Gly	Phe	Phe	Thr	Asp	
				55					60	
His	Ser	Trp	Tyr	Asn	Asp	Leu	Leu	Val	Arg	
				65					70	
Phe	Asp	Ser	Lys	Asp	Ile	Val	Asp	Lys	Tyr	
				75					80	
Lys	Gly	Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	
				85					90	
Tyr	Ala	Gly	Tyr	Gln	Cys	Ala	Gly	Gly	Thr	
				95					100	
Pro	Asn	Lys	Thr	Ala	Cys	Met	Tyr	Gly	Gly	
				105					110	
Val	Thr	Leu	His	Asp	Asn	Asn	Arg	Leu	Thr	
				115					120	
Glu	Glu	Lys	Lys	Val	Pro	Ile	Asn	Leu	Trp	
				125					130	
Leu	Asp	Gly	Lys	Gln	Asn	Thr	Val	Pro	Leu	
				135					140	
Glu	Thr	Val	Lys	Thr	Asn	Lys	Lys	Asn	Val	
				145					150	
Thr	Val	Gln	Glu	Leu	Asp	Leu	Gln	Ala	Arg	
				155					160	
Arg	Tyr	Leu	Gln	Glu	Lys	Tyr	Asn	Leu	Tyr	
				165					170	
Asn	Ser	Asp	Val	Phe	Asp	Gly	Lys	Val	Gln	
				175					180	
Arg	Gly	Leu	Ile	Val	Phe	His	Thr	Ser	Thr	
				185					190	
Glu	Pro	Ser	Val	Asn	Tyr	Asp	Leu	Phe	Gly	
				195					200	
Ala	Gln	Gly	Gln	Tyr	Ser	Asn	Thr	Leu	Leu	
				205					210	
Arg	Ile	Tyr	Arg	Asp	Asn	Lys	Thr	Ile	Asn	
				215					220	

Ser Glu Asn Met His Ile Asp Ile Tyr Leu
 225 230

Tyr Thr Ser

(6) INFORMATION FOR SEQUENCE ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAAGTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG	40
TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT	80
TACTTAATTT TAAAAGCATA ACTTAATTAA TATAAATAAC	120
ATGAGATTAT TAAATATAAT TAAGTTTCTT TTAATGTTTT	160
TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG	200
TATCTAGATA CTTTTTGGGA ATGTTGGATA AAGGAGATAA	240
AAAATGTATA AGAGATTATT TATTTACAT GTAATTTTGA	280
TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTTT	320
AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC	360
AAATCGAGTA AATTCACGG TTTGATGGAA GATATGAAAG	400
TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTTAA	440
ATCTATAGAT CAATTTCTAT ACTTTGACTT AATATATTCT	480
ATTAAGGACA CTAAGTTAGG GGATTATGAT AATGTTGAG	520
TCGAATTTAA AAACAAAGAT TTAGCTGATA AATACAAAGA	560
TAAATACGTA GATGTGTTG GAGCTAATTA TTATTATCAA	600
TGTTATTTTT CTAAAAAAC GAATGATATT AATTCGCATC	640
AAACTGACAA ACGAAAAACT TGTATGTATG GTGGTGTAAC	680

TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTTCGGG TATTTGAAGA TGGTAAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACCTGTC ACTATTTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACAA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCT GCACCAGGAG ATAAATTTGC CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCACCTTATA GAGTACCTGC CTTTTCTAAT	1120
ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAC CCCTTGTTGC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTTATCT TTACTATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTTCTCTTT	1280
TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTT CATTGATGTT TATTCTTGAC AAATCAATTC	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAATAATT	1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
CATTTGCTGT TTTATCGATA ATATTGCTT CTTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTTATTTCA	1560
GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAATAAAGC	1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT	1680
TTATTTTCTC CTATAACTTA TTTGCAATCG AT	1712

(7) INFORMATION FOR SEQUENCE ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val		
				5					10		
Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile		
				15					20		
Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln		
				25					30		
Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys		
				35					40		
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asp		
				45					50		
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val		
				55					60		
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln		
				65					70		
Phe	Leu	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile		
				75					80		
Lys	Asp	Thr	Lys	Leu	Gly	Asp	Tyr	Asp	Asn		
				85					90		
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu		
				95					100		
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp		
				105					110		
Val	Phe	Gly	Ala	Asn	Tyr	Tyr	Tyr	Gln	Cys		
				115					120		
Tyr	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn		
				125					130		
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys		
				135					140		

Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly	145	150
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr	155	160
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu	165	170
Leu	Ser	Phe	Asp	Val	Gln	Thr	Asn	Lys	Lys	175	180
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu	185	190
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys	195	200
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu	205	210
Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu	215	220
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala	225	230
Pro	Gly	Asp	Lys	Phe	Ala	Gln	Ser	Lys	Tyr	235	240
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val	245	250
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr	255	260
Leu	Thr	Thr	Lys	Lys	Lys					265	

(8) INFORMATION FOR SEQUENCE ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG

TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT	80
TACTTAATTT TAAAAGCATA ACTTAATTAA TATAAATAAC	120
ATGAGATTAT TAAATATAAT TAAGTTTCTT TTAATGTTTT	160
TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG	200
TATCTAGATA CTTTTTGGGA ATGTTGGATA AAGGAGATAA	240
AAAATGTATA AGAGATTATT TATTTACAT GTAATTTTGA	280
TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTTT	320
AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC	360
AAATCGAGTA AATTCACTGG TTTGATGGAA AATATGAAAG	400
TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTTAA	440
ATCTATAGAT CAATTTGAT ACTTTGACTT AATATATTCT	480
ATTAAGGACA CTAAGTTAGG GAATTATGAT AATGTTGAG	520
TCGAATTTAA AAACAAAGAT TTAGCTGATA AATACAAAGA	560
TAAATACGTA GATGTGTTTG GAGCTAATGC TTATTATCAA	600
TGTGCTTTTT CTAAAAAAC GAATGATATT AATTCGCATC	640
AAACTGACAA ACGAAAACT TGTATGTATG GTGGTGTAAC	680
TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTCTGGG TATTTGAAGA TGGTAAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACCTGTC ACTATTTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCT GCACCAGGAG ATAAATTTGA CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCACCTATA GAGTACCTGC CTTTCTAAT	1120

ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAC CCCTTGTTGC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTATCT TTAATATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTCTCTTT	1280
TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTT CATTGTTGATT TATCTTGAC AAATCAATTC	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAATAATT	1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
CATTTGCTGT TTTATCGATA ATATTGCTT CTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTATTTC	1560
GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAATAAAGC	1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT	1680
TTATTTTCTC CTATAACTTA TTTGCAATCG AT	1712

(9) INFORMATION FOR SEQUENCE ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Tyr Lys Arg Leu Phe Ile Ser His Val	
	5 10
Ile Leu Ile Phe Ala Leu Ile Leu Val Ile	
	15 20
Ser Thr Pro Asn Val Leu Ala Glu Ser Gln	
	25 30

Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys		
				35						40	
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asn		
				45						50	
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val		
				55						60	
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln		
				65						70	
Phe	Arg	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile		
				75						80	
Lys	Asp	Thr	Lys	Leu	Gly	Asn	Tyr	Asp	Asn		
				85						90	
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu		
				95						100	
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp		
				105						110	
Val	Phe	Gly	Ala	Asn	Ala	Tyr	Tyr	Gln	Cys		
				115						120	
Ala	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn		
				125						130	
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys		
				135						140	
Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly		
				145						150	
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr		
				155						160	
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu		
				165						170	
Leu	Ser	Phe	Asp	Val	Gln	Tyr	Asn	Lys	Lys		
				175						180	
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu		
				185						190	
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys		
				195						200	
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu		
				205						210	

Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu		
				215					220		
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala		
				225					230		
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr		
				235					240		
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val		
				245					250		
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr		
				255					260		
Leu	Thr	Thr	Lys	Lys	Lys						
				265							

(10) INFORMATION FOR SEQUENCE ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGTCAAC CAGATCCTAA ACCAGATGAG TTGCACAAAT	40
CGAGTAAATT CACTGGTTTG ATGGAAAATA TGAAAGTTTT	80
GTATGATGAT AATCATGTAT CAGCAATAAA CGTTAAATCT	120
ATAGATCAAT TTCGATACTT TGACTTAATA TATTCTATTA	160
AGGACACTAA GTTAGGGAAT TATGATAATG TTCGAGTCGA	200
ATTTAAAAAC AAAGATTTAG CTGATAAATA CAAAGATAAA	240
TACGTAGATG TGTTTGGAGC TAATGCTTAT TATCAATGTG	280
CTTTTCTAA AAAAACGAAT GATATTAATT CGCATCAAAC	320
TGACAAACGA AAAACTTGTA TGTATGGTGG TGTAAGTGG	360
CATAATGGAA ACCAATTAGA TAAATATAGA AGTATTACTG	400
TTCGGGTATT TGAAGATGGT AAAAATTTAT TATCTTTTGA	440

CGTACAAACT AATAAGAAAA AGGTGACTGC TCAAGAATTA	480
GATTACCTAA CTCGTCAC TAATTGGTGAAA AATAAAAAAC	520
TCTATGAATT TAACAACTCG CCTTATGAAA CGGGATATAT	560
TAAATTTATA GAAAATGAGA ATAGCTTTTG GTATGACATG	600
ATGCCTGCAC CAGGAGATAA ATTTGACCAA TCTAAATATT	640
TAATGATGTA CAATGACAAT AAAATGGTTG ATTCTAAAGA	680
TGTGAAGATT GAAGTTTATC TTACGACAAA GAAAAAGTGA	720
AATTATATTT TAGAAAAGTA AATATGAAGA GTTAGTAATT	760
AAGGCAGGCA CTTATAGAGT ACCTGCCTTT TCTAATATTA	800
TTTAGTTATA GTTATTTTTG TTATATCTCT CTGATTTAGC	840
ATTAACCCCT TGTGTCATT ATAGTTTTCAC CAACTTTAG	880
CTGAAATTGG GGGATCATTT TTATCTTTAC TATGGATAGT	920
TACTGTGTCG CCGTTTTTAA CGATTTGTTT CTCTTTTAAT	960
TTGTCAGTTA ATTTTTTCCA TGCATCATTT GCGTCAAACC	1000
TATTTCCATT TGGATTTATT CTTGACAAAT CAATTCTTTT	1040
AACACTATCG GTATTAATCG GCTTGTTATT AAAATTACTA	1080
AGTTCATCTA AATCAGCTGT ACCCGTAATA CTACTTTTCGC	1120
CACCATTATT TAAATTGTAC GTAACACCAA CTGTCTCATT	1160
TGCTGTTTTA TCGATAATAT TTGCTTCTTT CAAAGCATCT	1200
CTTACATTTT TCCATAAGTC TCTATCTGTT ATTTCAGAAG	1240
CCTTTGCAAC GTTATTAATA CCATTATAAT TTGAAGAAGA	1280
ATGAAAACCT GAACCTACTG TTGTTAAAAC TAAAGCACTT	1320
GCTATCAATG TTCTTGTTAA TAGTTTTTTA TTCATTTTAT	1360
TTTCTCCTAT AACTTATTTG CAATCGAT	1388

(11) INFORMATION FOR SEQUENCE ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239

(B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Pro Asp Pro Lys Pro Asp Glu
 5 10

Leu His Lys Ser Ser Lys Phe Thr Gly Leu
 15 20

Met Glu Asn Met Lys Val Leu Tyr Asp Asp
 25 30

Asn His Val Ser Ala Ile Asn Val Lys Ser
 35 40

Ile Asp Gln Phe Arg Tyr Phe Asp Leu Ile
 45 50

Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn
 55 60

Tyr Asp Asn Val Arg Val Glu Phe Lys Asn
 65 70

Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys
 75 80

Tyr Val Asp Val Phe Gly Ala Asn Ala Tyr
 85 90

Tyr Gln Cys Ala Phe Ser Lys Lys Thr Asn
 95 100

Asp Ile Asn Ser His Gln Thr Asp Lys Arg
 105 110

Lys Thr Cys Met Tyr Gly Gly Val Thr Glu
 115 120

His Asn Gly Asn Gln Leu Asp Lys Tyr Arg
 125 130

Ser Ile Thr Val Arg Val Phe Glu Asp Gly
 135 140

Lys Asn Leu Leu Ser Phe Asp Val Gln Thr
 145 150

Asn Lys Lys Lys Val Thr Ala Gln Glu Leu

	155		160
Asp Tyr Leu Thr Arg His Tyr Leu Val Lys			
	165		170
Asn Lys Lys Leu Tyr Glu Phe Asn Asn Ser			
	175		180
Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile			
	185		190
Glu Asn Glu Asn Ser Phe Trp Tyr Asp Met			
	195		200
Met Pro Ala Pro Gly Asp Lys Phe Asp Gln			
	205		210
Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn			
	215		220
Lys Met Val Asp Ser Lys Asp Val Lys Ile			
	225		230
Glu Val Tyr Leu Thr Thr Lys Lys Lys			
	235		

(12) INFORMATION FOR SEQUENCE ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAAGGAGAAT TAAAAATGAA TAAAAAATTA CTAATGAATT	40
TTTTTATCGT AAGCCCTTTG TTGCTTGCGA CAACTGCTAC	80
AGATTTTACC CCTGTTCCCT TATCATCTAA TCAAATAATC	120
AAAACTGCAA AAGCATCTAC AAACGATAAT ATAAAGGATT	160
TGCTAGACTG GTATAGTAGT GGGTCTGACA CTTTACAAA	200
TAGTGAAGTT TTAGATAATT CCAGAGGATC TATGCGTATA	240
AAAAACACAG ATGGCAGCAT CAGCTTGATA ATTTTCCGA	280

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GTCCTTATTA TAGCCCTGCT TTTACAAAAG GGGAAAAAGT    320
TGACTTAAAC ACAAAAAGAA CTAAAAAAG CCAACATACT    360
AGCGAAGGAA CTTATATCCA TTTCCAAATA AGTGGCGTTA    400
CAAATACTGA AAAATTACCT ACTCCAATAG AACTACCTTT    440
AAAAGTTAAG GTTCATGGTA AAGATAGCCC CTAAAGTAT    480
GGGCCAAAGT TCGATAAAAA ACAATTAGCT ATATCAACTT    520
TAGACTTTGA AATTCGTCAT CAGCTAACTC AAATACATGG    560
ATTATATCGT TCAAGCGATA AAACGGGTGG TTATTGAAA    600
ATAACAATGA ATGACGGATC CACATATCAA AGTGATTAT    640
CTAAAAAGTT TGAATACAAT ACTGAAAAAC CACCTATAAA    680
TATTGATGAA ATAAAACTA TAGAAGCAGA AATTAATTAA    720
TTTACCACTT T                                     731

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(13) INFORMATION FOR SEQUENCE ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Asn Lys Lys Leu Leu Met Asn Phe Phe
      5                               10

Ile Val Ser Pro Leu Leu Leu Ala Thr Thr
      15                           20

Ala Thr Asp Phe Thr Pro Val Pro Leu Ser
      25                           30

Ser Asn Gln Ile Ile Lys Thr Ala Lys Ala
      35                           40

Ser Thr Asn Asp Asn Ile Lys Asp Leu Leu
      45                           50

Asp Trp Tyr Ser Ser Gly Ser Asp Thr Phe
      55                           60

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Thr	Asn	Ser	Glu	Val	Leu	Asp	Asn	Ser	Arg	
				65					70	
Gly	Ser	Met	Arg	Ile	Lys	Asn	Thr	Asp	Gly	
				75					80	
Ser	Ile	Ser	Leu	Ile	Ile	Phe	Pro	Ser	Pro	
				85					90	
Tyr	Tyr	Ser	Pro	Ala	Phe	Thr	Lys	Gly	Glu	
				95					100	
Lys	Val	Asp	Leu	Asn	Thr	Lys	Arg	Thr	Lys	
				105					110	
Lys	Ser	Gln	His	Thr	Ser	Glu	Gly	Thr	Tyr	
				115					120	
Ile	His	Phe	Gln	Ile	Ser	Gly	Val	Thr	Asn	
				125					130	
Thr	Glu	Lys	Leu	Pro	Thr	Pro	Ile	Glu	Leu	
				135					140	
Pro	Leu	Lys	Val	Lys	Val	His	Gly	Lys	Asp	
				145					150	
Ser	Pro	Leu	Lys	Tyr	Gly	Pro	Lys	Phe	Asp	
				155					160	
Lys	Lys	Gln	Leu	Ala	Ile	Ser	Thr	Leu	Asp	
				165					170	
Phe	Glu	Ile	Arg	His	Gln	Leu	Thr	Gln	Ile	
				175					180	
His	Gly	Leu	Tyr	Arg	Ser	Ser	Asp	Lys	Thr	
				185					190	
Gly	Gly	Tyr	Trp	Lys	Ile	Thr	Met	Asn	Asp	
				195					200	
Gly	Ser	Thr	Tyr	Gln	Ser	Asp	Leu	Ser	Lys	
				205					210	
Lys	Phe	Glu	Tyr	Asn	Thr	Glu	Lys	Pro	Pro	
				215					220	
Ile	Asn	Ile	Asp	Glu	Ile	Lys	Thr	Ile	Glu	
				225					230	
Ala	Glu	Ile	Asn							

(14) INFORMATION FOR SEQUENCE ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

ATCATTAAT ATAATTAATT TTCTTTTAAT ATTTTTTTAA      40
TTGAATATTT AAGATTATAA GATATATTTA AAGTGATCT      80
AGATACTTTT TGGGAATGTT GGATGAAGGA GATAAAAATG     120
AATAAGAGTC GATTTATTTT ATGCGTAATT TTGATATTCG     160
CACTTATACT AGTTCTTTTT ACACCCAACG TATTAGCAGA     200
GAGCCAACCA GACCCTACGC CAGATGAGTT GCACAAAGCG     240
AGTAAATTCA CTGGTTTGAT GGAAAAATATG AAAGTTTTAT     280
ATGATGATCA TTATGTATCA GCAACTAAAG TTAAGTCTGT     320
AGATAAATTT AGGGCACATG ATTTAATTTA TAACATTAGT     360
GATAAAAAAC TGAAAAATTA TGACAAAAGTG AAAACAGAGT     400
TATTAAATGA AGGTTTAGCA AAGAAGTACA AAGATGAAGT     440
AGTTGATGTG TATGGATCAA ATTACTATGT AAACTGCTAT     480
TTTTCATCCA AAGATAATGT AGGTAAAGTT ACAGGTGGCA     520
AAACTTGTAT GTATGGAGGA ATAACAAAAC ATGAAGGAAA     560
CCACTTTGAT AATGGGAACT TACAAAATGT ACTTATAAGA     600
GTTTATGAAA ATAAAAGAAA CACAATTTCT TTTGAAGTGC     640
AAACTGATAA GAAAAGTGTA ACAGCTCAAG AACTAGACAT     680
AAAAGCTAGG AATTTTTTAA TTAATAAAAA AAATTTGTAT     720
GAGTTTAACA GTTCACCATA TGAAACAGGA TATATAAAAT     760
TTATTGAAAA TAACGGCAAT ACTTTTGGT ATGATATGAT     800

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GCCTGCACCA GCGATAAGT TTGACCAATC TAAATATTTA	840
ATGATGTACA ACGACAATAA AACGGTTGAT TCTAAAAGTG	880
TGAAGATAGA AGTCCACCTT ACAACAAAGA ATGGATAATG	920
TTAATCCGAT TTTGATATAA AAAGTGAAAG TATTAGATAT	960
ATTTGAAAGG TAAGTACTTC GGTGCTTGCC TTTTtaggAT	1000
GCATATATAT AGATTAAACC GCACTTCTAT ATTAATAGAA	1040
AGTGCGGTTA TTTATACACT CAATCTAAAC TATAATAATT	1080
GGAATCATCT TCAAA	1095

(15) INFORMATION FOR SEQUENCE ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Lys Ser Arg Phe Ile Ser Cys Val	
	5 10
Ile Leu Ile Phe Ala Leu Ile Leu Val Leu	
	15 20
Phe Thr Pro Asn Val Leu Ala Glu Ser Gln	
	25 30
Pro Asp Pro Thr Pro Asp Glu Leu His Lys	
	35 40
Ala Ser Lys Phe Thr Gly Leu Met Glu Asn	
	45 50
Met Lys Val Leu Tyr Asp Asp His Tyr Val	
	55 60
Ser Ala Thr Lys Val Lys Ser Val Asp Lys	
	65 70
Phe Arg Ala His Asp Leu Ile Tyr Asn Ile	
	75 80

Ser	Asp	Lys	Lys	Leu	Lys	Asn	Tyr	Asp	Lys	
				85					90	
Val	Lys	Thr	Glu	Leu	Leu	Asn	Glu	Gly	Leu	
				95					100	
Ala	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Val	Asp	
				105					110	
Val	Tyr	Gly	Ser	Asn	Tyr	Tyr	Val	Asn	Cys	
				115					120	
Tyr	Phe	Ser	Ser	Lys	Asp	Asn	Val	Gly	Lys	
				125					130	
Val	Thr	Gly	Gly	Lys	Thr	Cys	Met	Tyr	Gly	
				135					140	
Gly	Ile	Thr	Lys	His	Glu	Gly	Asn	His	Phe	
				145					150	
Asp	Asn	Gly	Asn	Leu	Gln	Asn	Val	Leu	Ile	
				155					160	
Arg	Val	Tyr	Glu	Asn	Lys	Arg	Asn	Thr	Ile	
				165					170	
Ser	Phe	Glu	Val	Gln	Thr	Asp	Lys	Lys	Ser	
				175					180	
Val	Thr	Ala	Gln	Glu	Leu	Asp	Ile	Lys	Ala	
				185					190	
Arg	Asn	Phe	Leu	Ile	Asn	Lys	Lys	Asn	Leu	
				195					200	
Tyr	Glu	Phe	Asn	Ser	Ser	Phe	Tyr	Glu	Thr	
				205					210	
Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Asn	Gly	
				215					220	
Asn	Thr	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala	
				225					230	
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr	
				235					240	
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Thr	Val	
				245					250	
Asp	Ser	Lys	Ser	Val	Lys	Ile	Glu	Val	His	
				255					260	

Leu Thr Thr Lys Asn Gly
265

(16) INFORMATION FOR SEQUENCE ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATGTTTGA CAGCTTATCA TCGATAAGCT TACTTTTTCGA	40
ATCAGGTCTA TCCTTGAAAC AGGTGCAACA TAGATTAGGG	80
CATGGAGATT TACCAGACAA CTATGAACGT ATATACTCAC	120
ATCACGCAAT CGGCAATTGA TGACATTGGA ACTAAATTCA	160
ATCAATTTGT TACTAACAAG CAACTAGATT GACAACTAAT	200
TCTCAACAAA CGTTAATTTA ACAACATTCA AGTAACTCCC	240
ACCAGCTCCA TCAATGCTTA CCGTAAGTAA TCATAACTTA	280
CTAAAACCTT GTTACATCAA GGTTTTTTCT TTTTGTCTTG	320
TTCATGAGTT ACCATAACTT TCTATATTAT TGACAACTAA	360
ATTGACAACT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT	400
TTCTTCATTT GATATAGTCT AATCCACCA TCACTTCTTC	440
CACTCTCTCT ACCGTCACAA CTTCATCATC TCTCACTTTT	480
TCGTGTGGTA ACACATAATC AAATATCTTT CCGTTTTTAC	520
GCACTATCGC TACTGTGTCA CCTAAAATAT ACCCCTTATC	560
AATCGCTTCT TTAAACTCAT CTATATATAA CATATTTTAT	600
CCTCCTACCT ATCTATTCGT AAAAAGATAA AAATAACTAT	640
TGTTTTTTTT GTTATTTTAT AATAAAATTA TTAATATAAG	680
TTAATGTTTT TTAAAAATAT ACAATTTTAT TCTATTTATA	720

GTTAGCTATT	TTTTCATTTGT	TAGTAATATT	GGTGAATTGT	760
AATAACCTTT	TTAAATCTAG	AGGAGAACCC	AGATATAAAA	800
TGGAGGAATA	TTAATGGAAA	ACAATAAAAA	AGTATTGAAG	840
AAAATGGTAT	TTTTTGTTTT	AGTGACATTT	CTTGGAATAA	880
CAATCTCGCA	AGAGGTATTT	GCTCAACAAG	ACCCCGATCC	920
AAGCCAACTT	CACAGATCTA	GTTTAGTTAA	AAACCTTCAA	960
AATATATATT	TTCTTTATGA	GGGTGACCCCT	GTTACTCACG	1000
AGAATGTGAA	ATCTGTTGAT	CAACTTAGAT	CTCACGATTT	1040
AATATATAAT	GTTTCAGGGC	CAAATTATGA	TAAATTAAAA	1080
ACTGAACTTA	AGAACCAAGA	GATGGCAACT	TTATTTAAGG	1120
ATAAAAACGT	TGATATTTAT	GGTGTAGAAT	ATTACCATCT	1160
CTGTTATTTA	TGTGAAAATG	CAGAAAGGAG	TGCATGTATC	1200
TACGGAGGGG	TAACAAATCA	TGAAGGGAAT	CATTTAGAAA	1240
TTCCATAAAA	GATAGTCGTT	AAAGTATCAA	TCGATGGTAT	1280
CCAAAGCCTA	TCATTTGATA	TTGAAACAAA	TAAAAAAAATG	1320
GTAACCTGCTC	AAGAATTAGA	CTATAAAGTT	AGAAAAATATC	1360
TTACAGATAA	TAAGCAACTA	TATACTAATG	GACCTTCTAA	1400
ATATGAAACT	GGATATATAA	AGTTCATACC	TAAGAATAAA	1440
GAAAGTTTTT	GGTTTGATTT	TTTCCCTGAA	CCAGAATTTA	1480
CTCAATCTAA	ATATCTTATG	ATATATAAAG	ATAATGAAAC	1520
GCTTGACTCA	AACACAAGCC	AAATTGAAGT	CTACCTAACA	1560
ACCAAGTAAC	TTTTTGCTTT	TGGCAACCTT	ACCTACTGCT	1600
GGATTTAGAA	ATTTTATTGC	AATTCCTTTA	TTAATGTAAA	1640
AACCGCTCAT	TTGATGAGCG	GTTTTGTCTT	ATCTAAAGGA	1680
GCTTTACCTC	CTAATGCTGC	AAAATTTTAA	ATGTTGGATT	1720
TTTGTATTTG	TCTATTGTAT	TTGATGGGTA	ATCCCATTTT	1760
TCGACAGACA	TCGTCGTGCC	ACCTCTAACA	CCAAAATCAT	1800

AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC

1837

(17) INFORMATION FOR SEQUENCE ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Asn Asn Lys Lys Val Leu Lys Lys
5 10

Met Val Phe Phe Val Leu Val Thr Phe Leu
15 20

Gly Leu Thr Ile Ser Gln Glu Val Phe Ala
25 30

Gln Gln Asp Pro Asp Pro Ser Gln Leu His
35 40

Arg Ser Ser Leu Val Lys Asn Leu Gln Asn
45 50

Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val
55 60

Thr His Glu Asn Val Lys Ser Val Asp Gln
65 70

Leu Arg Ser His Asp Leu Ile Tyr Asn Val
75 80

Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr
85 90

Glu Leu Lys Asn Gln Glu Met Ala Thr Leu
95 100

Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly
105 110

Val Glu Tyr Tyr His Leu Cys Tyr Leu Cys
115 120

Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr
125 130

Gly Gly Val Thr Asn His Glu Gly Asn His

	135		140
Leu Glu Ile Pro Lys Lys Ile Val Val Lys			
	145		150
Val Ser Ile Asp Gly Ile Gln Ser Leu Ser			
	155		160
Phe Asp Ile Glu Thr Asn Lys Lys Met Val			
	165		170
Thr Ala Gln Glu Leu Asp Tyr Lys Val Arg			
	175		180
Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr			
	185		190
Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly			
	195		200
Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu			
	205		210
Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro			
	215		220
Glu Phe Thr Gln Ser Lys Tyr Leu Met Ile			
	225		230
Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn			
	235		240
Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr			
	245		250

Lys

(18) INFORMATION FOR SEQUENCE ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser His Asp Gln Phe Leu Gln His Thr Ile		
	5	10
Leu Phe Lys Gly Phe Phe Thr Asp His Ser		
	15	20
Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp		
	25	30
Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly		
	35	40

Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	Tyr	Tyr		
				45						50	
Gly	Tyr	Gln	Cys	Ala	Gly	Gly	Thr	Pro	Asn		
				55						60	
Lys	Thr	Ala	Cys	Met	Tyr	Gly	Gly	Val	Thr		
				65						70	
Leu	His	Asp	Asn	Asn	Arg	Leu	Thr	Glu	Glu		
				75						80	
Lys	Lys										

(19) INFORMATION FOR SEQUENCE ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Thr	Gly	Asp	Gln	Phe	Leu	Glu	Asn	Thr	Leu		
				5						10	
Leu	Tyr	Lys	Lys	Phe	Phe	Thr	Asp	Leu	Ile		
				15						20	
Asn	Phe	Glu	Asp	Leu	Leu	Ile	Asn	Phe	Asn		
				25						30	
Ser	Lys	Glu	Met	Ala	Gln	His	Phe	Lys	Ser		
				35						40	
Lys	Asn	Val	Asp	Val	Tyr	Pro	Ile	Arg	Tyr		
				45						50	
Ser	Ile	Asn	Cys	Tyr	Gly	Gly	Glu	Ile	Asp		
				55						60	
Arg	Thr	Ala	Cys	Thr	Tyr	Gly	Gly	Val	Thr		
				65						70	
Pro	His	Glu	Gly	Asn	Lys	Leu	Lys	Glu	Arg		
				75						80	
Lys	Lys										

(20) INFORMATION FOR SEQUENCE ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Asp	Asp	Gln	Phe	Leu	Glu	Asn	Thr	Leu		
				5						10	
Leu	Phe	Lys	Gly	Phe	Phe	Thr	Gly	His	Pro		
				15						20	
Trp	Tyr	Asn	Asp	Leu	Leu	Val	Asp	Leu	Gly		
				25						30	
Ser	Lys	Asp	Ala	Thr	Asn	Lys	Tyr	Lys	Gly		
				35						40	
Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	Tyr	Tyr		
				45						50	

Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn
 55 60
 Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
 65 70
 Leu His Asp Asn Asn Arg Leu Thr Glu Glu
 75 80
 Lys Lys

(21) INFORMATION FOR SEQUENCE ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Ile Asp Gln Phe Leu Tyr Phe Asp Leu
 5 10
 Ile Tyr Ser Ile Lys Asp Thr Lys Leu Gly
 15 20
 Asn Tyr Asp Asn Val Arg Val Glu Phe Lys
 25 30
 Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp
 35 40
 Lys Tyr Val Asp Val Phe Gly Ala Asn Tyr
 45 50
 Tyr Gln Cys Tyr Phe Ser Lys Lys Thr Asn
 55 60
 Asp Ile Asn Ser His Gln Thr Asp Lys Arg
 65 70
 Lys Thr Cys Met Tyr Gly Gly Val Thr Glu
 75 80
 His Asn Gly Asn Gln Leu Asp Lys Tyr
 85

(22) INFORMATION FOR SEQUENCE ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys Phe Leu Ala His Asp Leu
 5 10
 Ile Tyr Asn Ile Ser Asp Lys Lys Leu Lys
 15 20
 Asn Tyr Asp Lys Val Lys Thr Glu Leu Leu
 25 30
 Asn Glu Gly Leu Ala Lys Lys Tyr Lys Asp
 35 40
 Glu Val Val Asp Val Tyr Gly Ser Asn Tyr
 45 50
 Tyr Val Asn Cys Tyr Phe Ser Ser Lys Asp

	55	60
Asn Val Gly Lys	Val Thr Gly Gly Lys Thr	
	65	70
Cys Met Tyr Gly	Gly Ile Thr Lys His Glu	
	75	80
Gly Asn His Phe	Asp Asn Gly Asn Leu	
	85	

(23) INFORMATION FOR SEQUENCE ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys	Phe Leu Ala His Asp Leu	
	5	10
Ile Tyr Asn Ile	Ser Asp Lys Lys Leu Lys	
	15	20
Asn Tyr Asp Lys	Val Lys Thr Glu Leu Leu	
	25	30
Asn Glu Asp Leu	Ala Lys Lys Tyr Lys Asp	
	35	40
Glu Val Val Asp	Val Tyr Gly Ser Asn Tyr	
	45	50
Tyr Val Asn Cys	Tyr Phe Ser Ser Lys Asp	
	55	60
Asn Val Gly Lys	Val Thr Gly Gly Lys Thr	
	65	70
Cys Met Tyr Gly	Gly Ile Thr Lys His Glu	
	75	80
Gly Asn His Phe	Asp Asn Gly Asn Leu	
	85	

(24) INFORMATION FOR SEQUENCE ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys	Phe Leu Ala His Asp Leu	
	5	10
Ile Tyr Asn Ile	Ser Asp Lys Lys Leu Lys	
	15	20
Asn Tyr Asp Lys	Val Lys Thr Glu Leu Leu	
	25	30
Asn Glu Asp Leu	Ala Lys Lys Tyr Lys Asp	
	35	40
Glu Val Val Asp	Val Tyr Gly Ser Asn Tyr	
	45	50
Tyr Val Asn Cys	Tyr Phe Ser Ser Lys Asp	
	55	60

Asn Val Gly Lys Val Thr Gly Gly Lys Thr
 65 70
 Cys Met Tyr Gly Gly Ile Thr Lys His Glu
 75 80
 Gly Asn His Phe Asp Asn Gly Asn Leu
 85

(25) INFORMATION FOR SEQUENCE ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Gln Leu Leu Ser His Asp Leu
 5 10
 Ile Tyr Asn Val Ser Gly Pro Asn Tyr Asp
 15 20
 Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
 25 30
 Met Ala Thr Leu Phe Lys Asp Lys Asn Val
 35 40
 Asp Ile Tyr Gly Val Glu Tyr Tyr His Leu
 45 50
 Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser
 55 60
 Ala Cys Ile Tyr Gly Gly Val Thr Asn His
 65 70
 Glu Gly Asn His Leu Glu Ile Pro Lys
 75

(26) INFORMATION FOR SEQUENCE ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Val Leu Asp Asn Ser Leu Gly Ser Met Arg
 5 10
 Ile Lys Asn Thr Asp Gly Ser Ile Ser Leu
 15 20
 Ile Ile Phe Pro Ser Pro Tyr Tyr Ser Pro
 25 30
 Ala Phe Thr Lys Gly Glu Lys Val Asp Leu
 35 40
 Asn Thr Lys Arg Thr Lys Lys Ser Gln His
 45 50
 Thr Ser Glu Gly Thr Tyr Ile His Phe Gln
 55 60
 Ile Ser Gly Val Thr Asn Thr Glu Lys Leu
 65 70
 Pro Thr Pro